Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application.

Listing of Claims:

Claims 1-20 (canceled)

Claim 21 (previously presented): A transgenic plant transformed with an expression vector comprising a polynucleotide sequence encoding a polypeptide having a conserved domain that has at least 70% sequence identity to the conserved domain of amino acid coordinates 111-164 of SEQ ID NO: 194.

Claim 22 (previously presented): The transgenic plant of claim 21, wherein the expression vector further comprises a constitutive, inducible, or tissue-specific promoter operably linked to the polynucleotide sequence.

Claim 23 (currently amended): ~~Seed~~ A seed produced by the transgenic plant according to claim 21, wherein the seed comprises the polynucleotide sequence of claim 21.

Claim 24 (currently amended): A method for producing a transgenic plant having an altered trait as compared to a wild-type plant of the same species, the method steps comprising:

(a) providing an expression vector comprising:

(i) a polynucleotide sequence encoding a polypeptide comprising a conserved domain that has at least 70% sequence identity to the conserved domain of amino acid coordinates 111-164 of SEQ ID NO: 194; and

(ii) at least one regulatory element operably linked to the polynucleotide sequence, wherein said at least one regulatory element controls expression of the polynucleotide sequence in a target plant;

(b) introducing the expression vector into at least one plant; and

(c) selecting at least one transgenic plant that has an altered trait as compared to a wild-type plant of the same species;

wherein the altered trait is selected from the group consisting of greater tolerance to cold during germination, greater tolerance to cold during growth, greater tolerance to ~~drought~~ water deprivation, greater tolerance to nitrogen limitation, larger leaves, and greater biomass than the wild-type plant.

Claim 25 (previously presented): The method of claim 24, wherein the polypeptide comprises a conserved domain that has at least 75% sequence identity to the conserved domain of amino acid coordinates 111-164 of SEQ ID NO: 194.

Claim 26 (previously presented): The method of claim 24, wherein the polypeptide comprises a conserved domain that has at least 80% sequence identity to the conserved domain of amino acid coordinates 111-164 of SEQ ID NO: 194.

Claim 27 (previously presented): The method of claim 24, wherein the regulatory element is a cauliflower mosaic virus 35S promoter.

Claim 28 (previously presented): The method of claim 24, wherein the regulatory element is a root-specific, epidermis-specific, meristem-specific, or leaf-specific promoter.

Claim 29 (previously presented): The method of claim 24, wherein the regulatory element is a drought-inducible or cold-inducible promoter.

Claim 30 (canceled)

Claim 31 (previously presented): The method of claim 24, wherein the transgenic plant has greater tolerance to 168 hours without watering than the wild-type plant.

Claim 32 (previously presented): The method of claim 24, wherein the transgenic plant has greater tolerance than the wild-type plant to six hours of exposure to 8° C during germination or six hours of exposure to 4° to 8° C during growth.

Claim 33 (previously presented): The method of claim 24, wherein the transgenic plant has greater tolerance than the wild-type plant to MS media with the nitrogen source reduced to 20 mg/l of NH_4NO_3.

Claim 34 (currently amended): ~~Seed~~ A seed produced by a transgenic plant produced by the method according to claim 24, wherein the seed comprises the expression vector of claim 24.

Claim 35 (currently amended): A method for increasing the tolerance of a plant to an abiotic stress, the method steps comprising:

(a) providing an expression vector comprising:

(i) a polynucleotide sequence encoding a polypeptide comprising a conserved domain that has at least 70% sequence identity to the conserved domain of amino acid coordinates 111-164 of SEQ ID NO: 194; and

(ii) at least one regulatory element flanking the polynucleotide sequence, wherein said at least one regulatory element controls expression of the polynucleotide sequence in a target plant;

(b) introducing the expression vector into a plant, thereby producing a transgenic plant; and

(c) selecting a transgenic plant having an altered trait as compared to a wild-type plant of the same species;

wherein the abiotic stress is selected from the group consisting of cold stress during germination, cold stress during growth, ~~drought stress~~ water deprivation, and nitrogen limitation.

Claim 36 (previously presented): The method of claim 35, wherein the polypeptide comprises a conserved domain that has at least 75% sequence identity to the conserved domain of amino acid coordinates 111-164 of SEQ ID NO: 194.

Claim 37 (previously presented): The method of claim 35, wherein the polypeptide comprises a conserved domain that has at least 80% sequence identity to the conserved domain of amino acid coordinates 111-164 of SEQ ID NO: 194.

Claim 38 (previously presented): The method of claim 35, wherein the transgenic plant has greater tolerance to 168 hours without watering than the wild-type plant.

Claim 39 (previously presented): The method of claim 35, wherein the transgenic plant has greater tolerance than the wild-type plant to six hours of exposure to 8° C during germination or six hours of exposure to 4° to 8° C during growth.

Claim 40 (previously presented): The method of claim 35, wherein the transgenic plant has greater tolerance than the wild-type plant to MS media with the nitrogen source reduced to 20 mg/l of NH_4NO_3.